



#5

032301.269.seq.ST25.txt
SEQUENCE LISTING

<110> Farwick, Mike, et al.

<120> PROCESS FOR THE PREPARATION OF L-AMINO ACIDS BY USING CORYNEFOR
M BACTERIA

<130> 032301 WN 269

<160> 6

<170> PatentIn version 3.1

<210> 1

<211> 2234

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (632)..(1660)

<223>

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20 1

tcttcttggc aagtgggtgg gacaggccaa atgcaccaac gtaggttgcc agcaggccag
80 1

tagctactgc aggacccttc ttttcattcc agcttcgtgc agcaagcgt ccgcatgctg
40 2

ccaatggaat ggtgcccagt gggcgaatgc cggattcacg ggcagtcaac caaccgccga
00 3

tcaaacctgc tgcgacgacg gtggcagtgc tgacctgga tgcctttttc aatttcattt
60 3

ccatggtgag ccagtctaga gacaaaattt ttccgcgggg gttttcttga tctgatccga
20 4

caaccgaatg ggggcaaaaa tgtgtccgac caaaaattgt gcagcacacc acatgcccg
80 4

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tccgacaatg tcgatttgtt aatgaaactg cagctctggc gattaaataa gatggtcaga 5
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gacagttttt tggcctgtca acccctgtga ttctcttatt tttgggtgat tgttccggcg 6
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cgggtgttgt gatgggttta atatggaaga c atg cga att gct act ctc acg 6
52

Met Arg Ile Ala Thr Leu Thr

1

5

tca ggc ggc gac tgc ccc gga cta aac gcc gtc atc cga gga atc gtc 7
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Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val Ile Arg Gly Ile Val

10

15

20

cgc aca gcc agc aat gaa ttt ggc tcc acc gtc gtt ggt tat caa gac 7
48

Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val Val Gly Tyr Gln Asp

25

30

35

ggt tgg gaa gga ctg tta ggc gat cgt cgc gta cag ctg tat gac gat 7
96

Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp

40

45

50

55

gaa gat att gac cga atc ctc ctt cga ggc ggc acc att ttg ggc act 8
44

Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr

60

65

70

ggt cgc ctc cat ccg gac aag ttt aag gcc gga att gat cag att aag 8
92

Gly Arg Leu His Pro Asp Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys

75

80

85

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gcc aac tta gaa gac gcc ggc atc gat gcc ctt atc cca atc ggt ggc	9
40 Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly	
90 95 100	
gaa gga acc ctg aag ggt gcc aag tgg ctg tct gat aac ggt atc cct	9
88 Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro	
105 110 115	
gtt gtc ggt gtc cca aag acc att gac aat gac gtg aat ggc act gac	10
36 Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp Val Asn Gly Thr Asp	
120 125 130 135	
ttc acc ttc ggt ttc gat act gct gtg gca gtg gct acc gac gct gtt	10
84 Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val Ala Thr Asp Ala Val	
140 145 150	
gac cgc ctg cac acc acc gct gaa tct cac aac cgt gtg atg atc gtg	11
32 Asp Arg Leu His Thr Thr Ala Glu Ser His Asn Arg Val Met Ile Val	
155 160 165	
gag gtc atg ggc cgc cac gtg ggt tgg att gct ctg cac gca ggt atg	11
80 Glu Val Met Gly Arg His Val Gly Trp Ile Ala Leu His Ala Gly Met	
170 175 180	
gcc ggc ggt gct cac tac acc gtt att cca gaa gta cct ttc gat att	12
28 Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu Val Pro Phe Asp Ile	
185 190 195	

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gca gag atc tgc aag gcg atg gaa cgt cgc ttc cag atg ggc gag aag 12
76

Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe Gln Met Gly Glu Lys

200 205 210 215

tac ggc att atc gtc gtt gcg gaa ggt gcg ttg cca cgc gaa ggc acc 13
24

Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr

220 225 230

atg gag ctt cgt gaa ggc cac att gac cag ttc ggt cac aag acc ttc 13
72

Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe Gly His Lys Thr Phe

235 240 245

acg gga att gga cag cag atc gct gat gag atc cac gtg cgc ctc ggc 14
20

Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile His Val Arg Leu Gly

250 255 260

68 cac gat gtt cgt acg acc gtt ctt ggc cac att caa cgt ggt gga acc 14

His Asp Val Arg Thr Thr Val Leu Gly His Ile Gln Arg Gly Gly Thr

265 270 275

cga act gct ttc gac cgt gtt ctg gcc act cgt tat ggt gtt cgt gca 15
16

Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg Tyr Gly Val Arg Ala

280 285 290 295

gct cgt gcg tgc cat gag gga agc ttt gac aag gtt gtt gct ttg aag 15
64

Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys Val Val Ala Leu Lys

300

305

310

ggt gag agc att gag atg atc acc ttt gaa gaa gca gtc gga acc ttg 16
12

Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu Ala Val Gly Thr Leu

315

320

325

aag gaa gtt cca ttc gaa cgc tgg gtt act gcc cag gca atg ttt gga 16
60

Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala Gln Ala Met Phe Gly

330

335

340

tagtttttcg ggcttttatac aacagccaat aacagctctt tcgcccattg aggtggaggg 17
20

gctgtttttt catgccgtaa ggaaagtgca agtaagtga atcaagtggc ctagatccat 17
80

tgacacttag actgtgacct aggcttgact ttcgtggggg agtggggata agttcatctt 18
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aaacacaatg caatcgattg catttacgtt ccttatccca caataggggt accttccaga 19
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aagttgggta ggagatggct tccgaaacct ccagcccgaa gaagcggggc accacgctca 19
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aagacatcgc gcaagcaaca cagctttcag tcagcacggg gtcccgggca ttggccaaca 20
20

acgcgagcat tccggaatcc acacgcatcc gagtgggtga agccgctcaa aagctgaact 20
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tcattccaaa cattgagaac ccatatttct cctcactagc agcatcgatt caaaaagctg 22
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032301.269.seq.ST25.txt

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 <213> Corynebacterium glutamicum

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 20 25 30

Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg
 35 40 45

Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg
 50 55 60

Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp Lys Phe Lys
 65 70 75 80

Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp
 85 90 95

Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp
 100 105 110

Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp
 115 120 125

Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val
 130 135 140

Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser
 145 150 155 160

His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp

165

170

175

Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile
 180 185 190

Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg
 195 200 205

Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly
 210 215 220

Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp
 225 230 235 240

Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp
 245 250 255

Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly
 260 265 270

His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala
 275 280 285

Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe
 290 295 300

Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe
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Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val
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<210> 3

032301.269.seq.ST25.txt

<211> 2160
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 <213> Corynebacterium glutamicum

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 <222> (609)..(1598)
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attttcctgg attcaggttt agcgtgcacg gcgattgcca cggtgttggg ggatcctcca 1
 80

gaagatgcca ggtggactgt tgttacaagt tccccggcg ctgtgattgc cttgtccgcg 2
 40

acagatgcca cctccacggt ggtgctgcac gggcaggttc acggtaattg ttcttcaatc 3
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attgggtcca cggcagtaga catgatttcg cagttgcgcg ctgatatcgc cttcgtggag 3
 60

gttgatgcga ttcaatccga tacaagtctg tgcacgtttt tcccggagac gattcccatc 4
 20

aagcaagcca tgatcaaaaa cgcggctttc acagttgctg ttctcagccc gagatctccc 4
 80

caagatcaag aacttcaact tttgaagcac cttttttcca cttgggctga ttttgatgcc 5
 40

cttgttaccg atgaccacac gctagatttt ccagttttgc ccgaccacaa ctttcaggtg 6
 00

gtaacccc atg atc atc aca ttc acc cca aac ccg agt att gat tcc acg 6
 50

Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr

1 5 10

032301.269.seq.ST25.txt

ctg tcg ctc ggc gaa gag ctc tcc cgt gga tcc gtc caa cga ctt gat 98				6
Leu Ser Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp				
15	20	25	30	
tcc gtc acc gct gtc gca ggt ggt aaa ggc atc aat gtc gcc cac gct 46				7
Ser Val Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala				
	35	40	45	
gtc ttg ctt gcg ggc ttt gaa acc ttg gct gtg ttc cca gcc ggc aag 94				7
Val Leu Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys				
	50	55	60	
ctc gac ccc ttc gtc cca ctg gtc cgc gac atc ggc ttg ccc gtg gaa 42				8
Leu Asp Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu				
	65	70	75	
act gtt gtg atc aac aag aac gtc cgc acc aac acc aca gtc acc gaa 90				8
Thr Val Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu				
	80	85	90	
ccg gac ggc acc acc acc aag ctc aac ggc ccc ggc gcg ccg ctc agc 38				9
Pro Asp Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser				
95	100	105	110	
gag cag aag ctc cgt agc ttg gaa aag gtg ctt atc gac gcg ctc cgc 86				9
Glu Gln Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg				
	115	120	125	

032301.269.seq.ST25.txt

ccc gaa gtc acc tgg gtt gtc ctg gcg ggc tcg ctg cca cca ggg gca 34 Pro Glu Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala	10
130 135 140	
cca gtt gac tgg tac gcg cgt ctc acc gcg ttg atc cat tca gca cgc 82 Pro Val Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg	10
145 150 155	
cct gac gtt cgc gtg gct gtc gat acc tca gac aag cca ctg atg gcg 30 Pro Asp Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala	11
160 165 170	
ttg ggc gag agc ttg gat aca cct ggc gct gct ccg aac ctg att aag 78 Leu Gly Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys	11
175 180 185 190	
cca aat ggt ctg gaa ctg ggc cag ctg gct aac act gat ggt gaa gag 26 Pro Asn Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu	12
195 200 205	
ctg gag gcg cgt gct gcg caa ggc gat tac gac gcc atc atc gca gct 74 Leu Glu Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala	12
210 215 220	
gcg gac gta ctg gtt aac cgt ggc atc gaa cag gtg ctt gtc acc ttg 22 Ala Asp Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu	13
225 230 235	

032301.269.seq.ST25.txt

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Gly Ala Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala	
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250	
act tct cca aag att gat gtt gta tcc acc gtt gga gct gga gac tgt 18	14
Thr Ser Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys	
255	260
265	270
gct ctt gca ggt ttt gtt atg gca cgt tcc cag aag aaa aca ctg gag 66	14
Ala Leu Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu	
275	280
285	
gaa tct ctg ctg aat gcc gtg tct tac ggc tcg act gcg gcg tct ctt 14	15
Glu Ser Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu	
290	295
300	
cct ggc act acc att cct cgt cct gac caa ctc gcc aca gct ggt gca 62	15
Pro Gly Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala	
305	310
315	
acg gtc acc caa gtc aaa gga ttg aaa gaa tca gca tgaatagcgt 08	16
Thr Val Thr Gln Val Lys Gly Leu Lys Glu Ser Ala	
320	325
330	
aaataattcc tcgcttgtcc ggctggatgt cgatttcggc gactccacca cggatgtcat 68	16
caacaacctt gccactgtta ttttcgacgc tggccgagct tcctccgccg acgcccttgc	17

28

caaagacgcg ctggatcgtg aagcaaagtc cggcaccggc gttcctggtc aagttgctat 17
88

ccccactgc cgttccgaag ccgtatctgt ccctaccttg ggctttgctc gcctgagcaa 18
48

gggtgtggac ttcagcggac ctgatggcga tgccaacttg gtgttcctca ttgcagcacc 19
08

tgctggcggc ggcaaagagc acctgaagat cctgtccaag cttgctcgct ccttggtgaa 19
68

gaaggatttc atcaaggctc tgcaggaagc caccaccgag caggaaatcg tcgacgttgt 20
28

cgatgccgtg ctcaaccag caccaaaaac caccgagcca gctgcagctc cggctgcggc 20
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<210> 4

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 4

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20 25 30

Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
35 40 45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
50 55 60

032301.269.seq.ST25.txt

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
65 70 75 80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
85 90 95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
100 105 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
115 120 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
130 135 140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
145 150 155 160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
165 170 175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
180 185 190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
195 200 205

Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
210 215 220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
225 230 235 240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
245 250 255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
 260 265 270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
 275 280 285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
 290 295 300

Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
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Thr Gln Val Lys Gly Leu Lys Glu Ser Ala
 325 330

<210> 5
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<210> 6
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 29